Amendments to the Claims:

This listing of claims replaces all prior versions and listings of claims in the application:

Listing of Claims:

1.-14. (Canceled)

15. (Currently amended) A method for producing an (S)-4-halo-3-hydroxybutyric acid ester derivative, the method comprising reacting an (R)-2-octanol dehydrogenase having a molecular weight of about 30,000 Da as determined by SDS-PAGE and about 83,000 Da as determined by gel filtration, or a microorganism producing the (R)-2-octanol dehydrogenase, with a 4-haloacetoacetic acid ester derivative to reduce the 4-haloacetoacetic acid ester derivative, wherein the (R)-2-octanol dehydrogenase is a polypeptide selected from the group from (a) to (e) below:

(a) a polypeptide encoded by a polynucleotide that hybridizes under stringent conditions with a nucleic acid probe consisting of the complement of the nucleotide sequence of SEQ ID NO: 1, wherein the stringent conditions comprise washing in 0.5 x SSC at 42°C;

(b) a polypeptide comprising an amino acid sequence at least 70% identical to the amino acid sequence of SEQ ID NO:2;

(c) a polypeptide comprising the amino acid sequence of SEQ ID NO:2;

(d) a polypeptide comprising ~~the~~ an amino acid sequence ~~of~~ that is a variant of SEQ ID NO:2 with up to 50 conservative amino acid substitutions; and

(e) a polypeptide comprising ~~the~~ an amino acid sequence ~~of~~ that is a variant of SEQ ID NO:2 with up to 10 conservative amino acid substitutions.

16. (Previously presented) The method of claim 15, wherein the microorganism is a transformant comprising a recombinant vector into which a polynucleotide encoding the (R)-2-octanol dehydrogenase is inserted.

17. (Canceled)

18. (Previously presented) The method of claim 15, wherein the 4-haloacetoacetic acid ester derivative is 4-chloroacetoacetic acid ethyl ester and wherein the (S)-4-halo-3-hydroxybutyric acid ester derivative is (S)-4-chloro-3-hydroxybutyric acid ethyl ester.

19. (Canceled)

20. (Canceled)

21. (Previously presented) The method of claim 15, the method further comprising converting an oxidized form of β-nicotinamide adenine dinucleotide into a reduced form thereof.

22. (Canceled)

23. (Canceled)

24. (Canceled)

25. (Previously presented) The method of claim 15, wherein the (R)-2-octanol dehydrogenase has an optimal pH for the reduction reaction in a range from 5.0 to 6.5.

26. (Previously presented) The method of claim 15, wherein the reacting step is carried out with the microorganism producing the (R)-2-octanol dehydrogenase, and said microorganism belongs to the genus *Candida* or the genus *Ogataea*.

27. (Previously presented) The method of claim 15, wherein the reacting step is carried out with the microorganism producing the (R)-2-octanol dehydrogenase, and the microorganism belongs to the genus *Pichia*.

28. (Currently amended) The method of claim 15, wherein the (R)-2-octanol dehydrogenase is ~~substantially~~ at least 75% pure, ~~chemically~~ treated with an organic solvent, or in a cell-free extract.

29. (Previously presented) The method of claim 15, further comprising using a reduced form of β-nicotinamide adenine dinucleotide (NADH) as a coenzyme.

30. (Currently amended) The method of claim 15, wherein the (R)-2-octanol dehydrogenase is encoded by a polynucleotide that hybridizes under stringent conditions with a nucleic acid probe consisting of the complement of the nucleotide sequence of SEQ ID NO: 1, wherein the stringent conditions comprise washing in 0.5 x SSC at 42°C.

31. (Previously presented) The method of claim 15, wherein the (R)-2-octanol dehydrogenase comprises an amino acid sequence at least 70% identical to the amino acid sequence of SEQ ID NO: 2.

32. (Previously presented) The method of claim 31, wherein the (R)-2-octanol dehydrogenase comprises an amino acid sequence at least 80% identical to the amino acid sequence of SEQ ID NO: 2.

33. (Previously presented) The method of claim 31, wherein the (R)-2-octanol dehydrogenase comprises an amino acid sequence at least 90% identical to the amino acid sequence of SEQ ID NO: 2.

34. (Previously presented) The method of claim 31, wherein the (R)-2-octanol dehydrogenase comprises an amino acid sequence at least 95% identical to the amino acid sequence of SEQ ID NO: 2.

35. (Previously presented) The method of claim 15, wherein the (R)-2-octanol dehydrogenase comprises the amino acid sequence of SEQ ID NO: 2.

36. (Previously presented) The method of claim 35, wherein the (R)-2-octanol dehydrogenase consists of the amino acid sequence of SEQ ID NO: 2.

37. (Currently amended) The method of claim 15, wherein the (R)-2-octanol dehydrogenase comprises ~~the~~ an amino acid sequence ~~of~~ that is a variant of SEQ ID NO:2 with up to 50 conservative amino acid substitutions.

38. (Currently amended) The method of claim 15, wherein the (R)-2-octanol dehydrogenase comprises ~~the~~ an amino acid sequence ~~of~~ that is a variant of SEQ ID NO:2 with up to 10 conservative amino acid substitutions.

Please add new claims 39-47:

39. (New) The method of claim 15, wherein the (R)-2-octanol dehydrogenase comprises an amino acid sequence that is a variant of SEQ ID NO:2 with up to 30 conservative amino acid substitutions.

40. (New) A method for producing an (S)-4-halo-3-hydroxybutyric acid ester derivative, the method comprising reacting (i) a *Pichia* (R)-2-octanol dehydrogenase, or a microorganism producing the *Pichia* (R)-2-octanol dehydrogenase, with (ii) a 4-haloacetoacetic acid ester derivative to reduce the 4-haloacetoacetic acid ester derivative, wherein the (R)-2-octanol dehydrogenase oxidizes the S form of (R)-2-octanol with an activity of 50 or less when taking the activity on R form as 100.

41. (New) The method of claim 40, wherein the (R)-2-octanol dehydrogenase is a polypeptide selected from the group from (a) to (c) below:

(a) a polypeptide encoded by a polynucleotide that hybridizes under stringent conditions with a nucleic acid probe consisting of the complement of the nucleotide sequence of SEQ ID NO: 1, wherein the stringent conditions comprise washing in 0.5 x SSC at 42°C;

(b) a polypeptide comprising an amino acid sequence at least 70% identical to the amino acid sequence of SEQ ID NO:2; and

(c) a polypeptide comprising an amino acid sequence that is a variant of SEQ ID NO:2 with up to 50 conservative amino acid substitutions.

42. (New) The method of claim 40, wherein the *Pichia* is *Pichia finlandica*.

43. (New) The method of claim 40, wherein the *Pichia* is *Pichia jadinii*.

44. (New) A method for producing an (S)-4-halo-3-hydroxybutyric acid ester derivative, the method comprising reacting (i) a *Candida or Ogatae* (R)-2-octanol dehydrogenase, or a microorganism producing the *Candida or Ogatae* (R)-2-octanol dehydrogenase, with (ii) a 4-haloacetoacetic acid ester derivative to reduce the 4-haloacetoacetic acid ester derivative, and wherein the (R)-2-octanol dehydrogenase oxidizes the S form of (R)-2-octanol with an activity of 50 or less when taking the activity on R form as 100.

45. (New) The method of claim 44, wherein the (R)-2-octanol dehydrogenase is a polypeptide selected from the group from (a) to (c) below:

(a) a polypeptide encoded by a polynucleotide that hybridizes under stringent conditions with a nucleic acid probe consisting of the complement of the nucleotide sequence of SEQ ID NO: 1, wherein the stringent conditions comprise washing in 0.5 x SSC at 42°C;

(b) a polypeptide comprising an amino acid sequence at least 70% identical to the amino acid sequence of SEQ ID NO:2; and

(c) a polypeptide comprising an amino acid sequence that is a variant of SEQ ID NO:2 with up to 50 conservative amino acid substitutions.

46. (New) The method of claim 44, wherein the *Candida* is *Candida utilis*.

47. (New) The method of claim 44, wherein the *Ogataea* is *Ogataea wickerhamii*.